



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:48 AM UTC

PDB ID : 6IBM / pdb_00006ibm
Title : Crystal structure of human alpha-galactosidase A in complex with alpha-galactose configured cyclosulfate ME776
Authors : Rowland, R.J.; Wu, L.; Davies, G.J.
Deposited on : 2018-11-30
Resolution : 2.07 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

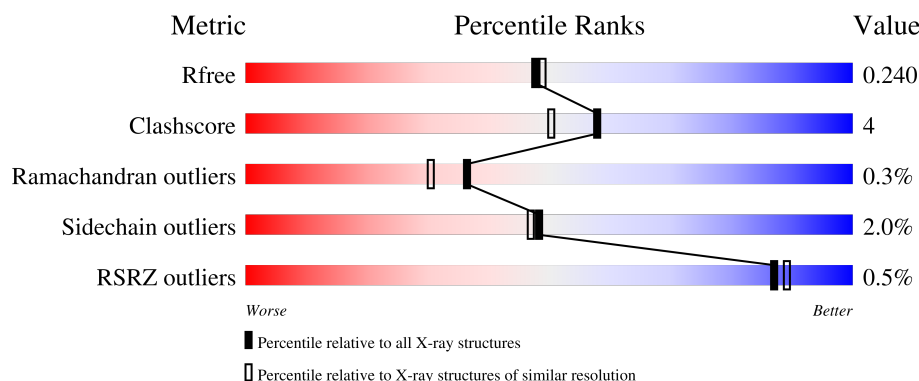
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	398	85% 13% ..
1	B	398	% 88% 10% .
2	C	3	100%
2	E	3	67% 33%
2	H	3	33% 67%

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Mol	Chain	Length	Quality of chain
3	D	2	 100%
3	G	2	 100%
4	F	6	 67% 33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PEG	A	509	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 6948 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Alpha-galactosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	3	0
			3139	1998	537	578	26			
1	B	392	Total	C	N	O	S	0	0	0
			3128	1992	532	577	27			

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



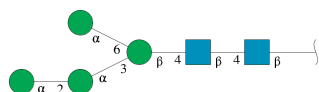
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	E	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	H	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



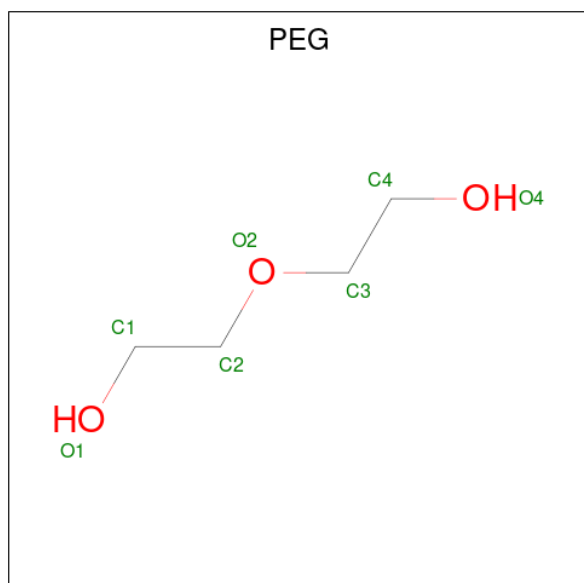
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



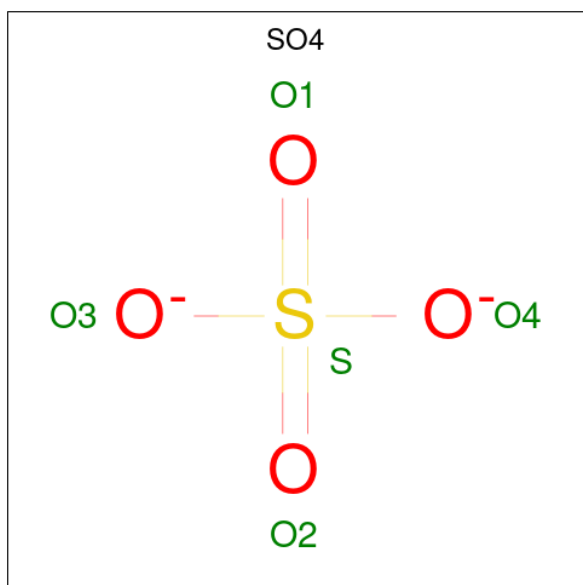
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



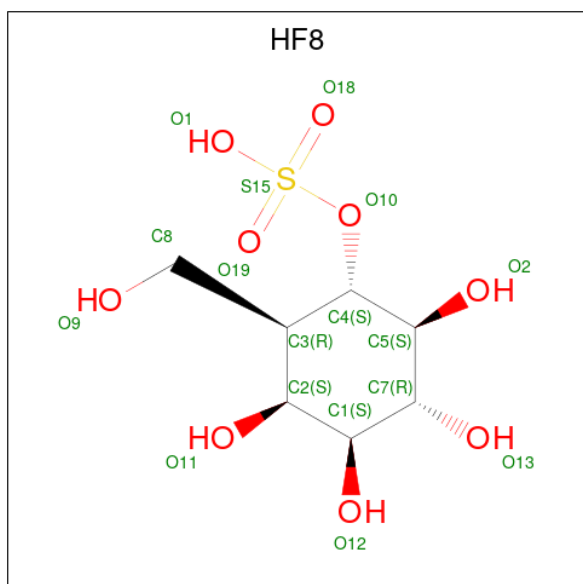
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is [(1 {S},2 {R},3 {S},4 {S},5 {R},6 {S})-2-(hydroxymethyl)-3,4,5,6-tetrakis(oxidanyl)cyclohexyl] hydrogen sulfate (CCD ID: HF8) (formula: C₇H₁₄O₉S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	O	S	0	0
			16	7	8	1		
8	B	1	Total	C	O	S	0	0
			16	7	8	1		

- Molecule 9 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			4	2	2		
9	A	1	Total	C	O	0	0
			4	2	2		
9	A	1	Total	C	O	0	0
			4	2	2		
9	A	1	Total	C	O	0	0
			4	2	2		
9	A	1	Total	C	O	0	0
			4	2	2		
9	A	1	Total	C	O	0	0
			4	2	2		
9	A	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		
9	B	1	Total	C	O	0	0
			4	2	2		

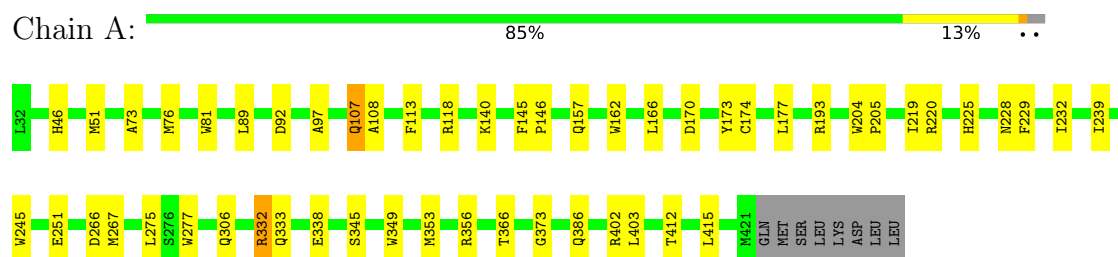
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	157	Total	O	0	0
			157	157		
10	B	115	Total	O	0	0
			115	115		

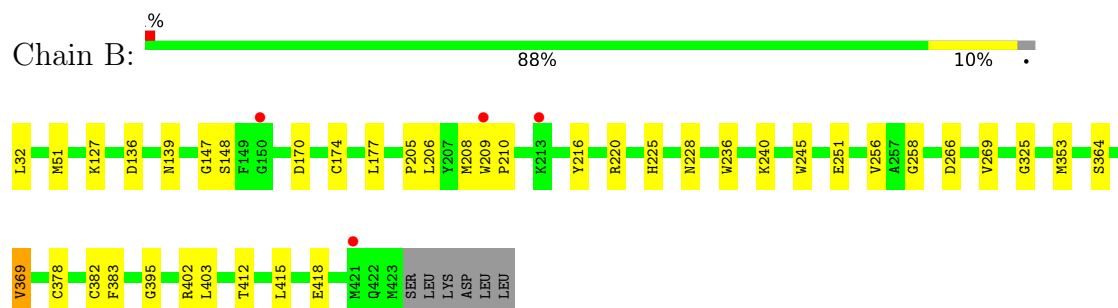
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Alpha-galactosidase A



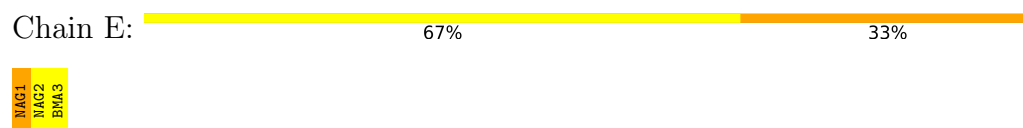
- Molecule 1: Alpha-galactosidase A



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  33% 67%

MAG1
MAG2
BMA3

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%

MAG1
MAG2

- Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  67% 33%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	90.34Å 90.34Å 216.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	78.36 – 2.07 78.24 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.9 (78.36-2.07) 100.0 (78.24-2.07)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.07Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.180 , 0.242 0.186 , 0.240	Depositor DCC
R_{free} test set	3073 reflections (3.04%)	wwPDB-VP
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6948	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, SO4, PEG, MAN, ACT, EDO, HF8

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.01	1/3226 (0.0%)	1.27	3/4382 (0.1%)
1	B	1.05	1/3215 (0.0%)	1.33	3/4368 (0.1%)
All	All	1.03	2/6441 (0.0%)	1.30	6/8750 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	170	ASP	CG-OD2	10.57	1.45	1.25
1	A	170	ASP	CG-OD2	10.08	1.44	1.25

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	220	ARG	CG-CD-NE	-6.36	98.01	112.00
1	B	269	VAL	N-CA-C	-5.30	107.56	112.43
1	A	229	PHE	CA-C-N	5.28	128.34	120.90
1	A	229	PHE	C-N-CA	5.28	128.34	120.90
1	B	174	CYS	CA-C-N	5.26	127.28	120.44
1	B	174	CYS	C-N-CA	5.26	127.28	120.44

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3139	0	2979	34	0
1	B	3128	0	2971	24	0
2	C	39	0	34	0	0
2	E	39	0	34	1	0
2	H	39	0	34	0	0
3	D	28	0	25	0	0
3	G	28	0	25	0	0
4	F	72	0	61	0	0
5	A	14	0	20	5	0
6	A	12	0	9	1	0
6	B	4	0	3	0	0
7	A	15	0	0	1	0
7	B	15	0	0	1	0
8	A	16	0	0	0	0
8	B	16	0	0	0	0
9	A	36	0	54	0	0
9	B	36	0	54	0	0
10	A	157	0	0	2	0
10	B	115	0	0	0	0
All	All	6948	0	6303	58	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (58) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:VAL:HG13	1:B:378:CYS:SG	2.25	0.77
1:A:403:LEU:HD21	1:A:415:LEU:CD1	2.22	0.69
1:B:209:TRP:N	1:B:210:PRO:HD2	2.15	0.62
1:A:277:TRP:H	5:A:509:PEG:C3	2.13	0.62
1:A:403:LEU:HD21	1:A:415:LEU:HD11	1.84	0.60
1:A:402:ARG:NH2	7:A:514:SO4:O1	2.31	0.59
1:A:251:GLU:H	1:A:251:GLU:CD	2.11	0.58
1:A:338:GLU:OE2	1:A:356:ARG:NH1	2.37	0.58
1:B:403:LEU:HD21	1:B:415:LEU:CD1	2.35	0.57
1:B:403:LEU:HD21	1:B:415:LEU:HD13	1.86	0.57
1:B:177:LEU:H	1:B:177:LEU:HD12	1.69	0.57
1:A:46:HIS:CD2	1:A:92:ASP:H	2.25	0.54
1:A:228:ASN:HB3	1:A:245:TRP:CH2	2.41	0.54
1:A:277:TRP:H	5:A:509:PEG:H31	1.72	0.54
1:B:208:MET:C	1:B:210:PRO:HD2	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:LEU:N	1:B:220:ARG:O	2.42	0.53
1:A:204:TRP:HB3	1:A:205:PRO:HD3	1.90	0.53
1:A:239:ILE:HD11	1:A:275:LEU:HD11	1.90	0.53
1:A:345:SER:HA	6:A:512:ACT:H2	1.91	0.52
1:A:332:ARG:HD2	10:A:724:HOH:O	2.10	0.51
1:B:369:VAL:CG1	1:B:378:CYS:CB	2.88	0.51
1:A:277:TRP:CZ3	1:A:306:GLN:HG2	2.47	0.49
1:B:216:TYR:HB3	1:B:256:VAL:HG11	1.94	0.49
1:A:97:ALA:HB3	1:A:107:GLN:HG3	1.94	0.49
1:B:228:ASN:HB3	1:B:245:TRP:CH2	2.47	0.49
1:B:139:ASN:C	1:B:147:GLY:HA3	2.38	0.48
1:B:353:MET:O	1:B:412:THR:HA	2.14	0.47
1:B:369:VAL:CG1	1:B:378:CYS:SG	2.98	0.47
1:A:157:GLN:NE2	10:A:607:HOH:O	2.48	0.46
1:A:366:THR:HA	1:A:403:LEU:O	2.16	0.46
1:A:205:PRO:HG3	1:A:219:ILE:HD13	1.97	0.46
1:A:73:ALA:HB2	1:A:89:LEU:CD2	2.46	0.46
1:A:76:MET:HA	1:A:81:TRP:HB2	1.98	0.45
1:A:118:ARG:H	5:A:510:PEG:H21	1.82	0.45
1:B:136:ASP:O	1:B:148:SER:HB2	2.17	0.45
1:A:386:GLN:HA	1:A:415:LEU:HD23	1.98	0.44
1:B:383:PHE:CE1	1:B:395:GLY:HA2	2.52	0.44
1:A:174:CYS:HA	2:E:1:NAG:H81	1.99	0.44
1:A:277:TRP:CB	5:A:509:PEG:H31	2.48	0.44
1:B:177:LEU:HD12	1:B:177:LEU:N	2.30	0.44
1:A:108:ALA:HB1	1:A:113:PHE:HB2	1.98	0.43
1:A:145:PHE:HB3	1:A:146:PRO:HD2	2.00	0.43
1:A:239:ILE:CD1	1:A:275:LEU:HD11	2.48	0.43
1:B:177:LEU:H	1:B:177:LEU:CD1	2.30	0.42
1:A:232:ILE:HD13	1:A:267:MET:O	2.19	0.42
1:A:349:TRP:CZ3	1:A:373:GLY:HA2	2.54	0.42
1:B:205:PRO:O	1:B:209:TRP:CD1	2.73	0.42
1:B:382:CYS:HA	1:B:418:GLU:O	2.20	0.42
1:B:236:TRP:NE1	1:B:240:LYS:HD2	2.36	0.41
1:B:209:TRP:N	1:B:210:PRO:CD	2.82	0.41
1:A:166:LEU:HD23	1:A:166:LEU:C	2.46	0.41
1:A:277:TRP:HB3	5:A:509:PEG:H31	2.02	0.41
1:A:140:LYS:HB2	1:A:173:TYR:CD2	2.56	0.40
1:A:353:MET:O	1:A:412:THR:HA	2.21	0.40
1:A:118:ARG:HA	1:A:162:TRP:O	2.21	0.40
1:B:258:GLY:HA2	1:B:325:GLY:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:ARG:NH2	7:B:513:SO4:O3	2.55	0.40
1:B:206:LEU:HA	1:B:209:TRP:HD1	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	391/398 (98%)	378 (97%)	12 (3%)	1 (0%)	36	30
1	B	390/398 (98%)	372 (95%)	17 (4%)	1 (0%)	36	30
All	All	781/796 (98%)	750 (96%)	29 (4%)	2 (0%)	36	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	266	ASP
1	A	266	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	330/339 (97%)	322 (98%)	8 (2%)	43	40
1	B	330/339 (97%)	324 (98%)	6 (2%)	51	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	660/678 (97%)	646 (98%)	14 (2%)	48 45

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51[A]	MET
1	A	51[B]	MET
1	A	107	GLN
1	A	177	LEU
1	A	193	ARG
1	A	225	HIS
1	A	332	ARG
1	A	333	GLN
1	B	51	MET
1	B	127	LYS
1	B	225	HIS
1	B	251	GLU
1	B	364	SER
1	B	369	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	HIS
1	B	107	GLN
1	B	406	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

19 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	C	1	2,1	14,14,15	0.66	0	17,19,21	1.02	1 (5%)
2	NAG	C	2	2	14,14,15	0.53	0	17,19,21	1.37	3 (17%)
2	BMA	C	3	2	11,11,12	0.48	0	15,15,17	1.11	1 (6%)
3	NAG	D	1	1,3	14,14,15	0.43	0	17,19,21	1.21	1 (5%)
3	NAG	D	2	3	14,14,15	0.41	0	17,19,21	1.63	6 (35%)
2	NAG	E	1	2,1	14,14,15	0.55	0	17,19,21	1.13	1 (5%)
2	NAG	E	2	2	14,14,15	0.41	0	17,19,21	1.05	1 (5%)
2	BMA	E	3	2	11,11,12	0.46	0	15,15,17	1.17	1 (6%)
4	NAG	F	1	4,1	14,14,15	0.45	0	17,19,21	1.19	3 (17%)
4	NAG	F	2	4	14,14,15	0.57	0	17,19,21	0.86	0
4	BMA	F	3	4	11,11,12	0.42	0	15,15,17	0.70	0
4	MAN	F	4	4	11,11,12	0.46	0	15,15,17	1.04	1 (6%)
4	MAN	F	5	4	11,11,12	0.27	0	15,15,17	0.59	0
4	MAN	F	6	4	11,11,12	0.69	0	15,15,17	0.98	0
3	NAG	G	1	1,3	14,14,15	0.48	0	17,19,21	1.04	1 (5%)
3	NAG	G	2	3	14,14,15	0.31	0	17,19,21	1.25	2 (11%)
2	NAG	H	1	2,1	14,14,15	0.50	0	17,19,21	1.28	2 (11%)
2	NAG	H	2	2	14,14,15	0.66	0	17,19,21	1.52	1 (5%)
2	BMA	H	3	2	11,11,12	0.45	0	15,15,17	1.02	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	1/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	MAN	F	4	4	-	1/2/19/22	0/1/1/1
4	MAN	F	5	4	-	1/2/19/22	0/1/1/1
4	MAN	F	6	4	-	2/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	3/6/23/26	0/1/1/1
2	BMA	H	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	2	NAG	C2-N2-C7	4.66	129.15	122.90
2	E	3	BMA	C1-O5-C5	3.59	116.99	112.19
2	C	2	NAG	O4-C4-C5	3.10	116.95	109.32
3	G	1	NAG	C1-C2-N2	3.02	115.19	110.43
2	E	1	NAG	C1-O5-C5	2.78	115.91	112.19
4	F	4	MAN	O2-C2-C1	2.76	115.55	109.22
2	C	3	BMA	O5-C5-C6	2.70	112.91	107.66
2	H	1	NAG	O7-C7-N2	2.66	126.69	121.98
3	G	2	NAG	O5-C5-C6	2.61	112.74	107.66
2	C	2	NAG	C3-C4-C5	-2.58	105.55	110.23
3	D	2	NAG	C1-O5-C5	2.57	115.63	112.19
3	D	2	NAG	O4-C4-C3	-2.52	104.43	110.38
2	E	2	NAG	O4-C4-C3	-2.47	104.55	110.38
2	H	1	NAG	C2-N2-C7	2.40	126.11	122.90
3	D	2	NAG	O3-C3-C4	-2.36	104.80	110.38
3	D	2	NAG	C2-N2-C7	-2.35	119.75	122.90
2	C	2	NAG	O4-C4-C3	-2.34	104.85	110.38
3	D	2	NAG	C3-C4-C5	2.34	114.47	110.23
4	F	1	NAG	C6-C5-C4	-2.33	107.29	113.02
3	D	2	NAG	C1-C2-N2	2.33	114.10	110.43
2	C	1	NAG	C4-C3-C2	-2.27	107.69	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2	NAG	C1-O5-C5	2.19	115.12	112.19
4	F	1	NAG	C1-C2-N2	2.08	113.71	110.43
4	F	1	NAG	O5-C1-C2	-2.03	108.15	111.29
3	D	1	NAG	O4-C4-C3	-2.01	105.64	110.38

There are no chirality outliers.

All (18) torsion outliers are listed below:

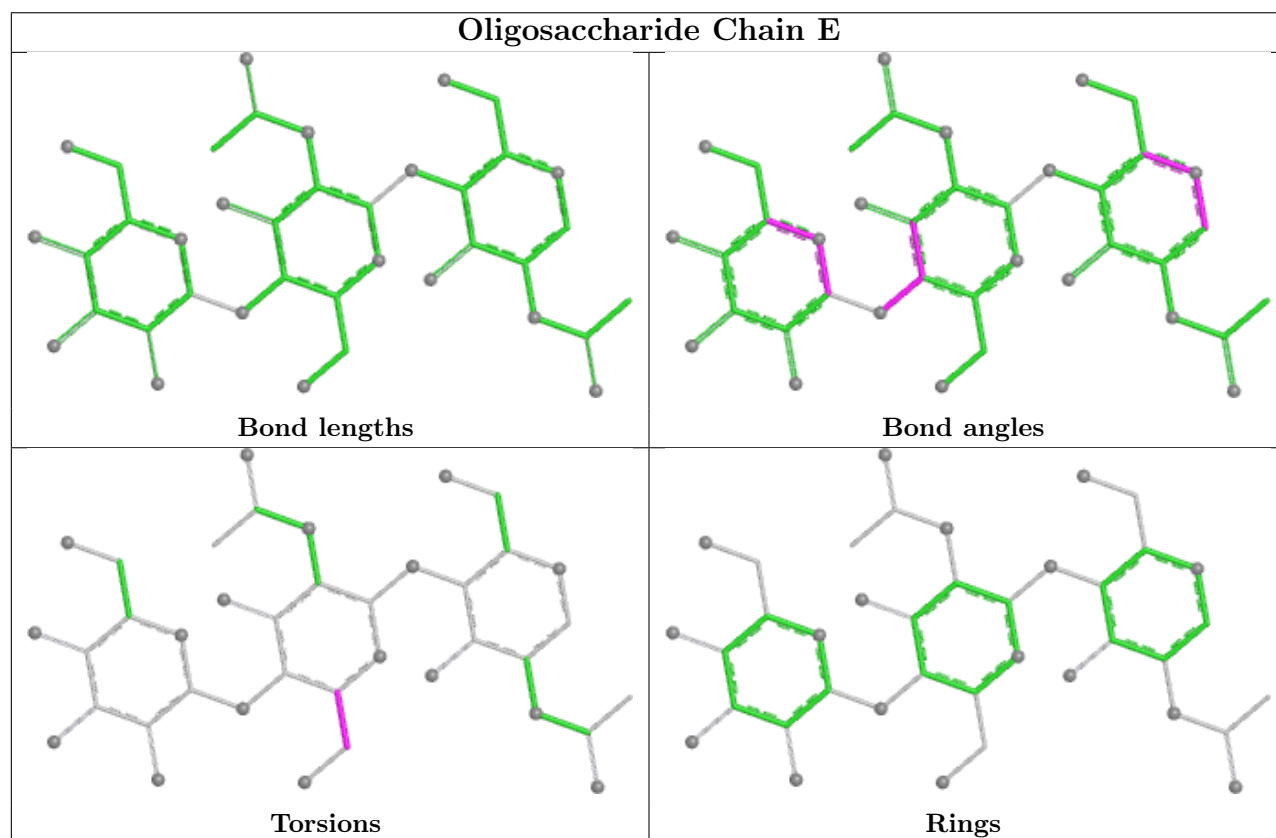
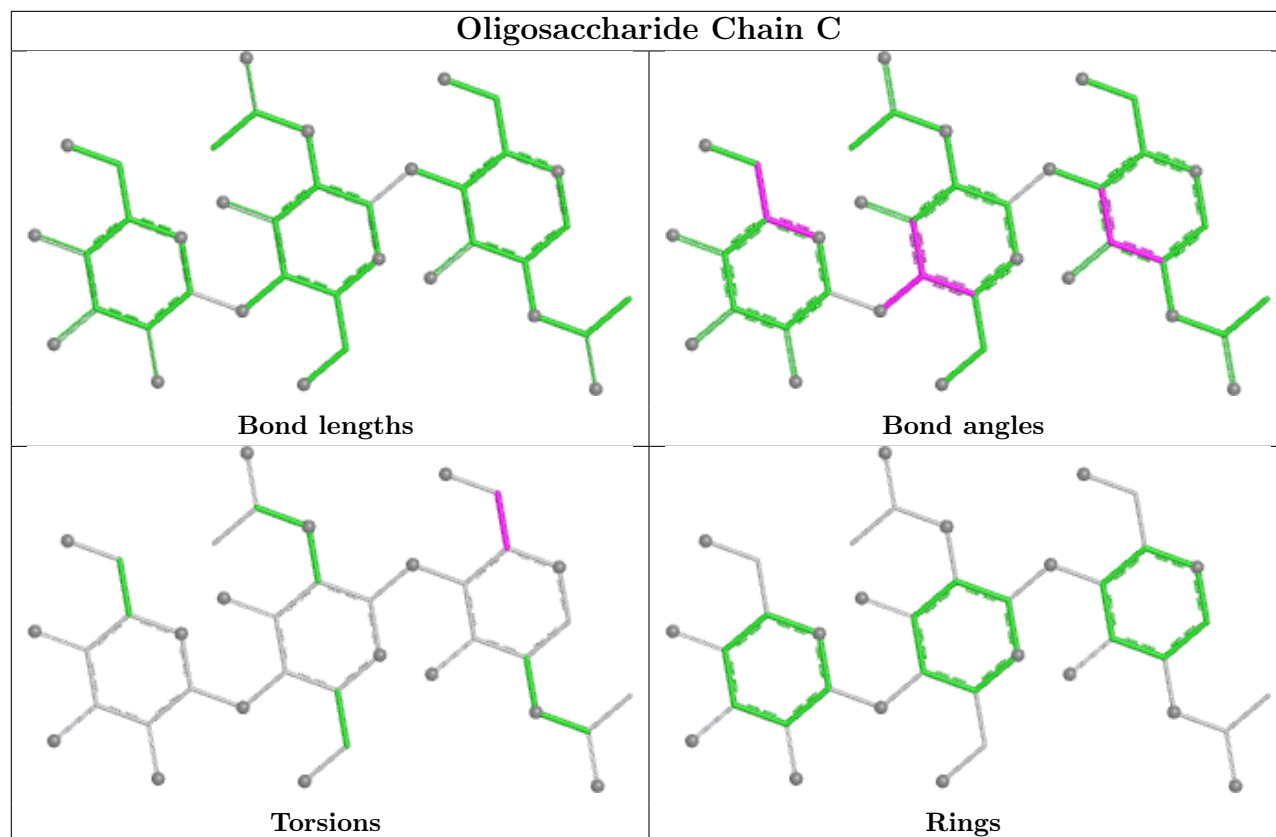
Mol	Chain	Res	Type	Atoms
2	H	2	NAG	C3-C2-N2-C7
4	F	6	MAN	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	H	2	NAG	C4-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	H	2	NAG	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
4	F	6	MAN	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
4	F	5	MAN	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
3	G	2	NAG	C3-C2-N2-C7
3	G	2	NAG	C1-C2-N2-C7
4	F	2	NAG	C1-C2-N2-C7
4	F	4	MAN	C4-C5-C6-O6

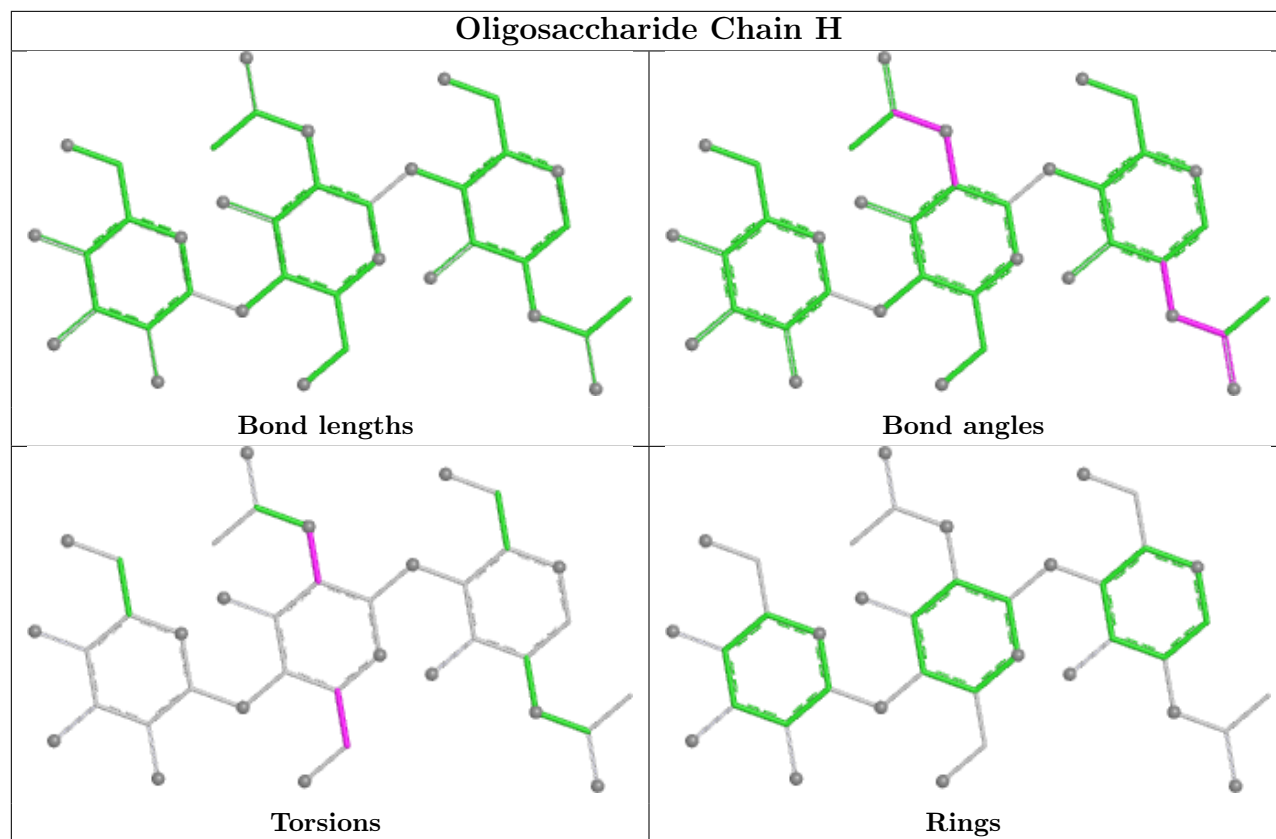
There are no ring outliers.

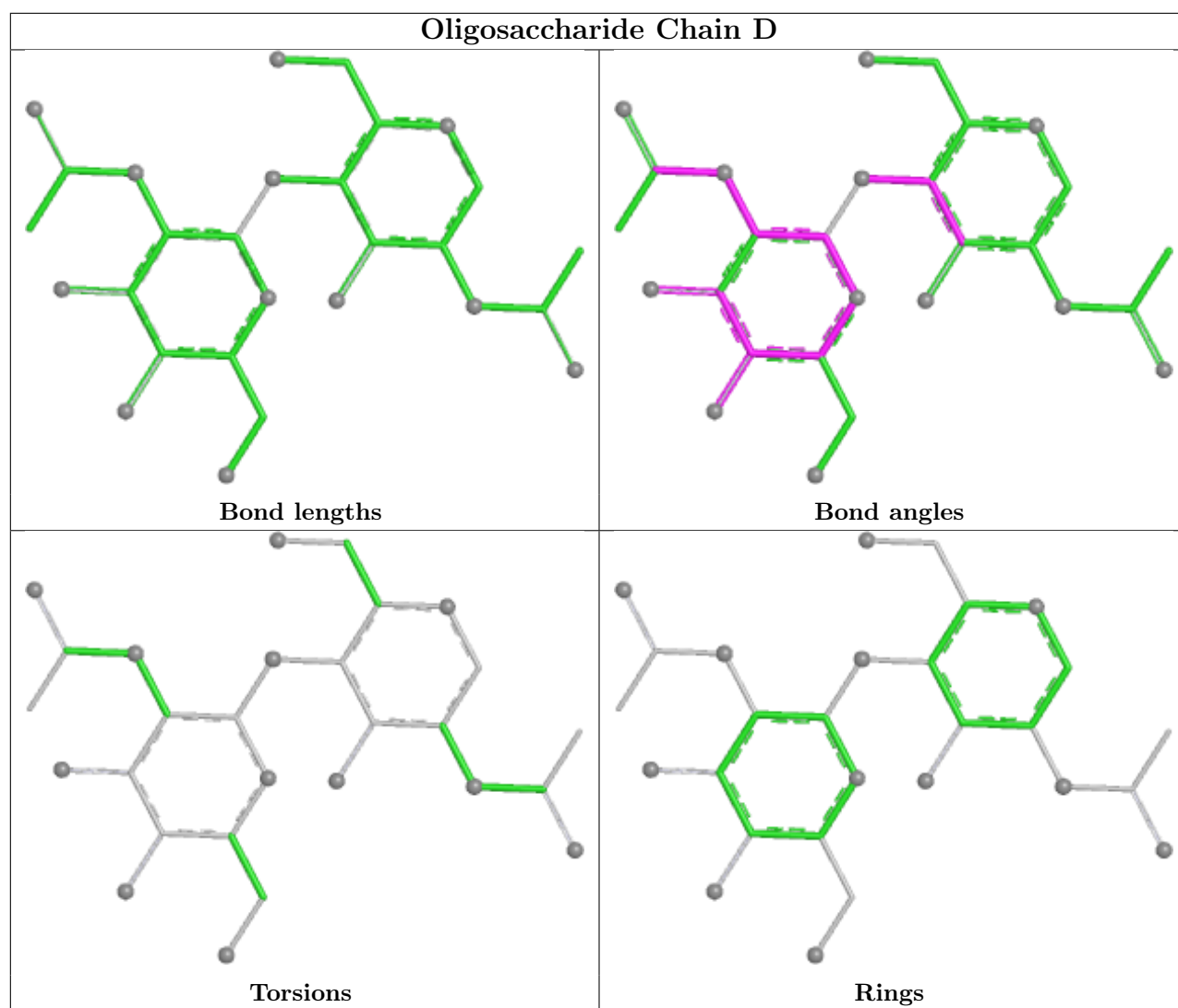
1 monomer is involved in 1 short contact:

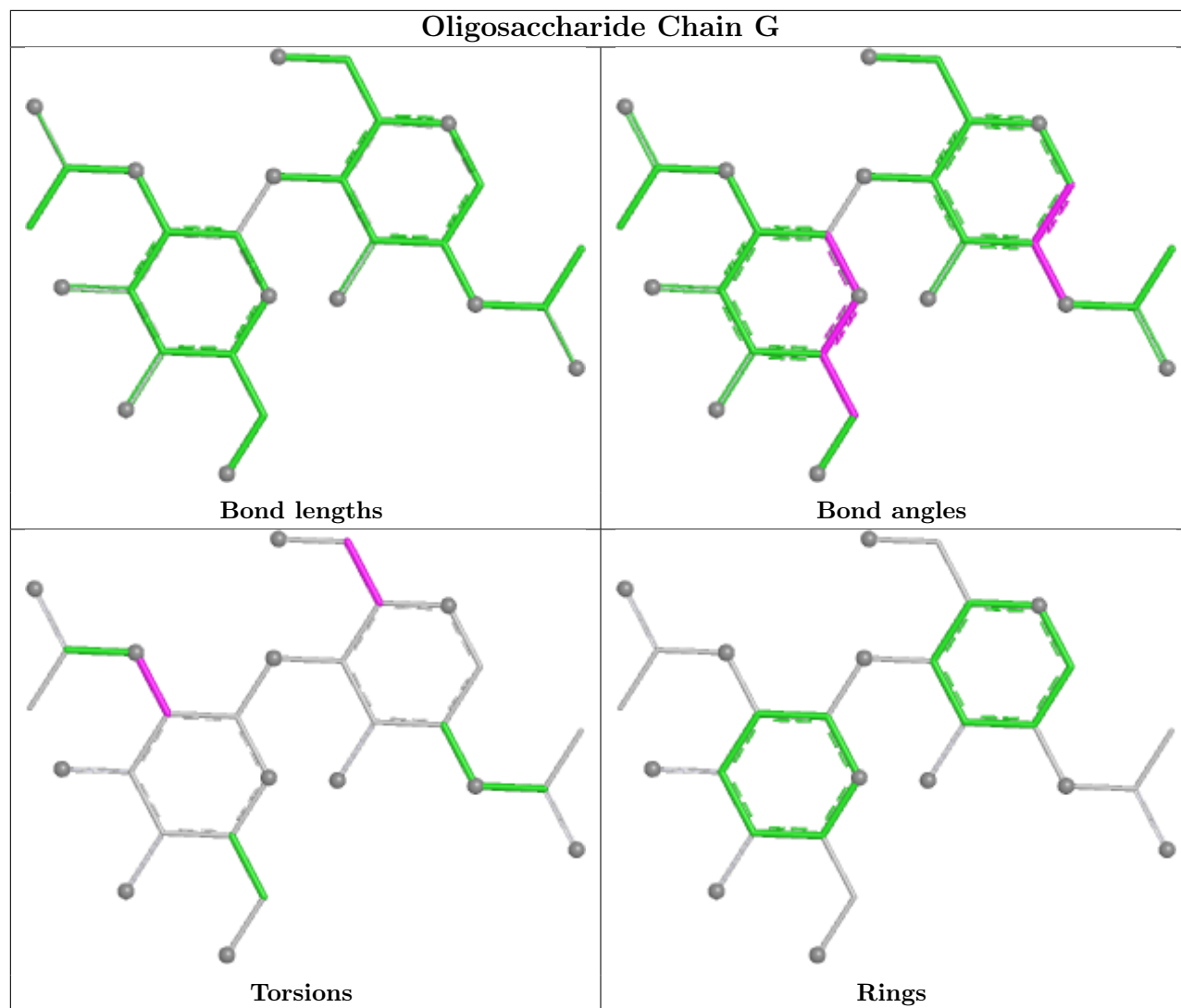
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0

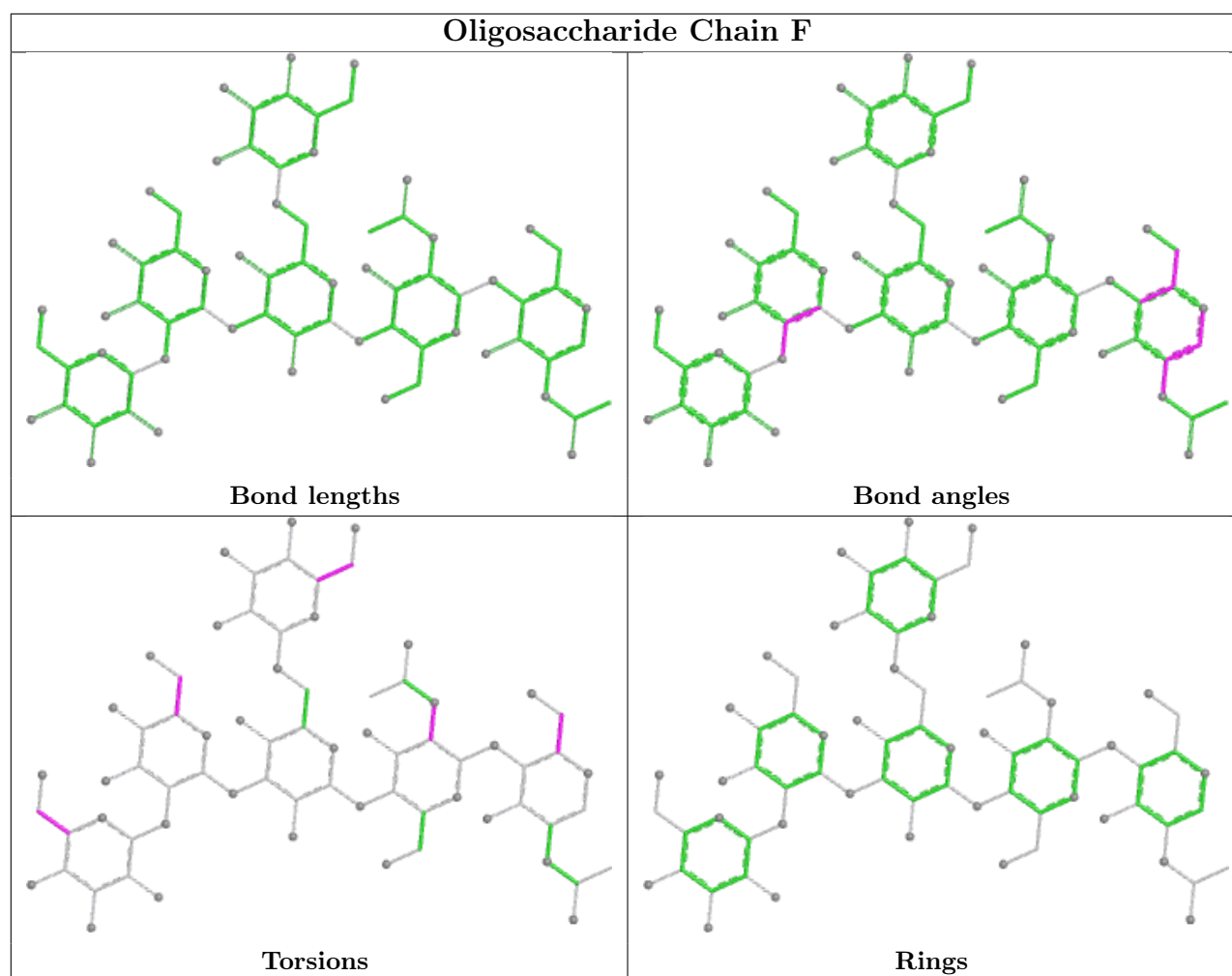
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	PEG	A	510	-	6,6,6	0.53	0	5,5,5	0.40	0
9	EDO	A	522	-	3,3,3	0.21	0	2,2,2	0.35	0
9	EDO	B	519	-	3,3,3	0.13	0	2,2,2	0.14	0
6	ACT	B	512	-	3,3,3	0.99	0	3,3,3	0.87	0
8	HF8	A	517	1	16,16,17	1.13	1 (6%)	17,24,26	1.18	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SO4	B	515	-	4,4,4	0.32	0	6,6,6	0.10	0
9	EDO	A	526	-	3,3,3	0.29	0	2,2,2	0.20	0
7	SO4	B	514	-	4,4,4	0.42	0	6,6,6	0.18	0
9	EDO	B	520	-	3,3,3	0.10	0	2,2,2	0.04	0
7	SO4	B	513	-	4,4,4	0.45	0	6,6,6	0.18	0
9	EDO	B	521	-	3,3,3	0.13	0	2,2,2	0.25	0
9	EDO	B	523	-	3,3,3	0.41	0	2,2,2	0.55	0
9	EDO	A	518	-	3,3,3	0.39	0	2,2,2	0.21	0
7	SO4	A	515	-	4,4,4	0.26	0	6,6,6	0.18	0
6	ACT	A	512	-	3,3,3	1.18	0	3,3,3	0.47	0
7	SO4	A	514	-	4,4,4	0.41	0	6,6,6	0.14	0
9	EDO	A	523	-	3,3,3	0.04	0	2,2,2	0.15	0
5	PEG	A	509	-	6,6,6	0.16	0	5,5,5	0.29	0
9	EDO	A	524	-	3,3,3	0.15	0	2,2,2	0.23	0
9	EDO	A	520	-	3,3,3	0.15	0	2,2,2	0.08	0
7	SO4	A	516	-	4,4,4	0.31	0	6,6,6	0.10	0
9	EDO	A	525	-	3,3,3	0.15	0	2,2,2	0.26	0
9	EDO	B	524	-	3,3,3	0.11	0	2,2,2	0.13	0
9	EDO	A	521	-	3,3,3	0.22	0	2,2,2	0.31	0
9	EDO	B	522	-	3,3,3	0.06	0	2,2,2	0.02	0
9	EDO	B	517	-	3,3,3	0.03	0	2,2,2	0.13	0
8	HF8	B	516	1	16,16,17	0.88	1 (6%)	17,24,26	1.32	3 (17%)
6	ACT	A	513	-	3,3,3	1.31	0	3,3,3	0.66	0
9	EDO	B	525	-	3,3,3	0.13	0	2,2,2	0.27	0
6	ACT	A	511	-	3,3,3	1.07	0	3,3,3	0.83	0
9	EDO	A	519	-	3,3,3	0.11	0	2,2,2	0.47	0
9	EDO	B	518	-	3,3,3	0.16	0	2,2,2	0.21	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	A	510	-	-	2/4/4/4	-
9	EDO	A	522	-	-	1/1/1/1	-
9	EDO	B	519	-	-	1/1/1/1	-
8	HF8	A	517	1	-	1/7/27/31	0/1/1/1
9	EDO	A	526	-	-	1/1/1/1	-
9	EDO	B	520	-	-	0/1/1/1	-
9	EDO	B	521	-	-	1/1/1/1	-
9	EDO	B	523	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	EDO	A	518	-	-	1/1/1/1	-
9	EDO	A	523	-	-	0/1/1/1	-
5	PEG	A	509	-	-	2/4/4/4	-
9	EDO	A	524	-	-	1/1/1/1	-
9	EDO	A	520	-	-	1/1/1/1	-
9	EDO	A	525	-	-	0/1/1/1	-
9	EDO	B	524	-	-	1/1/1/1	-
9	EDO	A	521	-	-	1/1/1/1	-
9	EDO	B	522	-	-	1/1/1/1	-
9	EDO	B	517	-	-	1/1/1/1	-
8	HF8	B	516	1	-	1/7/27/31	0/1/1/1
9	EDO	B	525	-	-	1/1/1/1	-
9	EDO	A	519	-	-	0/1/1/1	-
9	EDO	B	518	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	517	HF8	O10-C4	-3.95	1.41	1.47
8	B	516	HF8	O10-C4	-2.33	1.43	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	517	HF8	O10-C4-C5	-3.03	102.53	108.61
8	B	516	HF8	O10-C4-C5	-3.00	102.59	108.61
8	B	516	HF8	O11-C2-C3	2.77	115.59	109.94
8	B	516	HF8	O11-C2-C1	-2.21	105.16	110.38

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	526	EDO	O1-C1-C2-O2
5	A	510	PEG	C1-C2-O2-C3
5	A	510	PEG	O1-C1-C2-O2
9	A	520	EDO	O1-C1-C2-O2
9	A	522	EDO	O1-C1-C2-O2
9	A	524	EDO	O1-C1-C2-O2
9	B	524	EDO	O1-C1-C2-O2
9	B	517	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
5	A	509	PEG	O2-C3-C4-O4
8	B	516	HF8	C3-C4-O10-S15
5	A	509	PEG	C4-C3-O2-C2
9	A	518	EDO	O1-C1-C2-O2
9	B	519	EDO	O1-C1-C2-O2
9	B	522	EDO	O1-C1-C2-O2
9	B	525	EDO	O1-C1-C2-O2
9	A	521	EDO	O1-C1-C2-O2
9	B	521	EDO	O1-C1-C2-O2
8	A	517	HF8	C3-C4-O10-S15

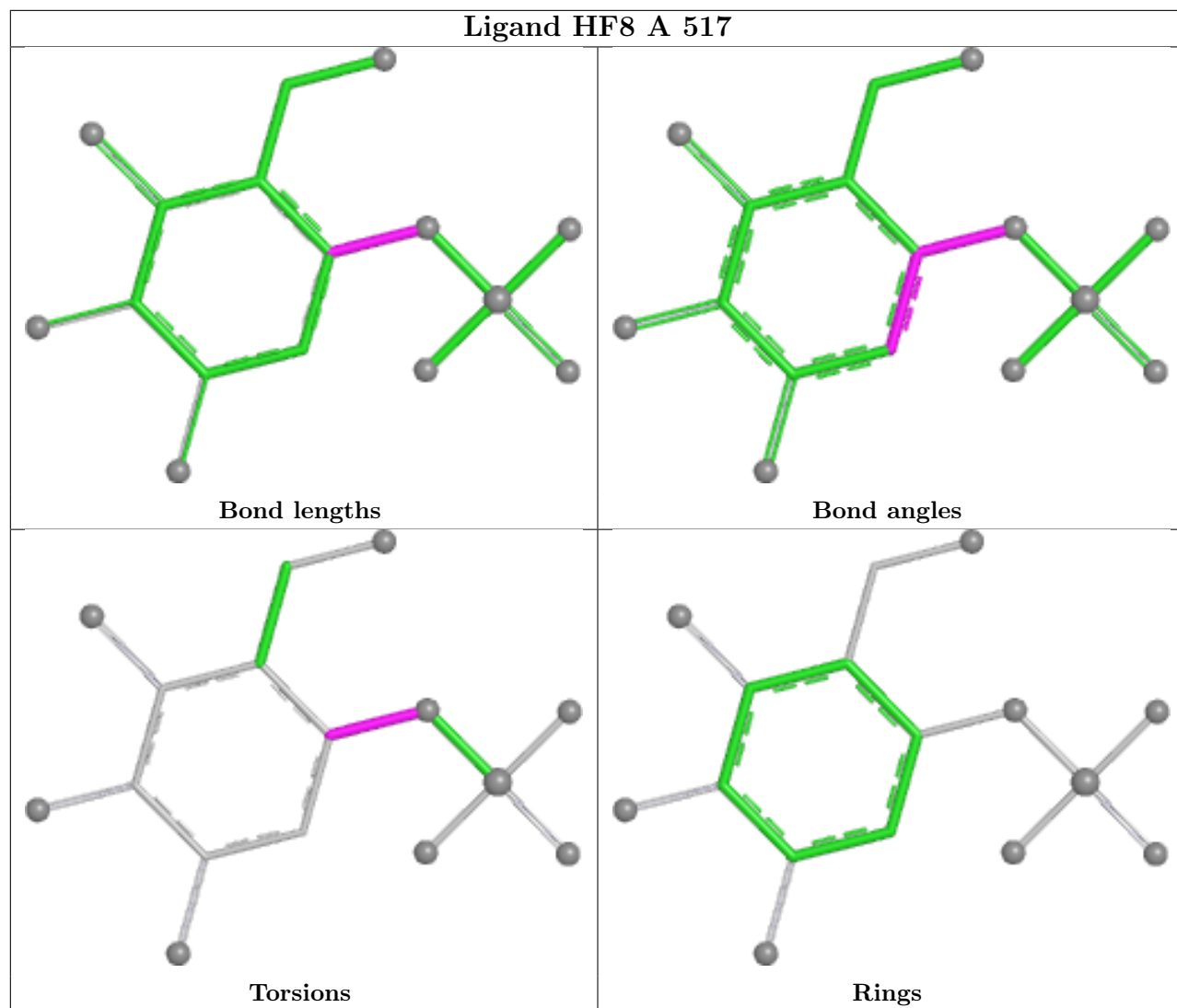
There are no ring outliers.

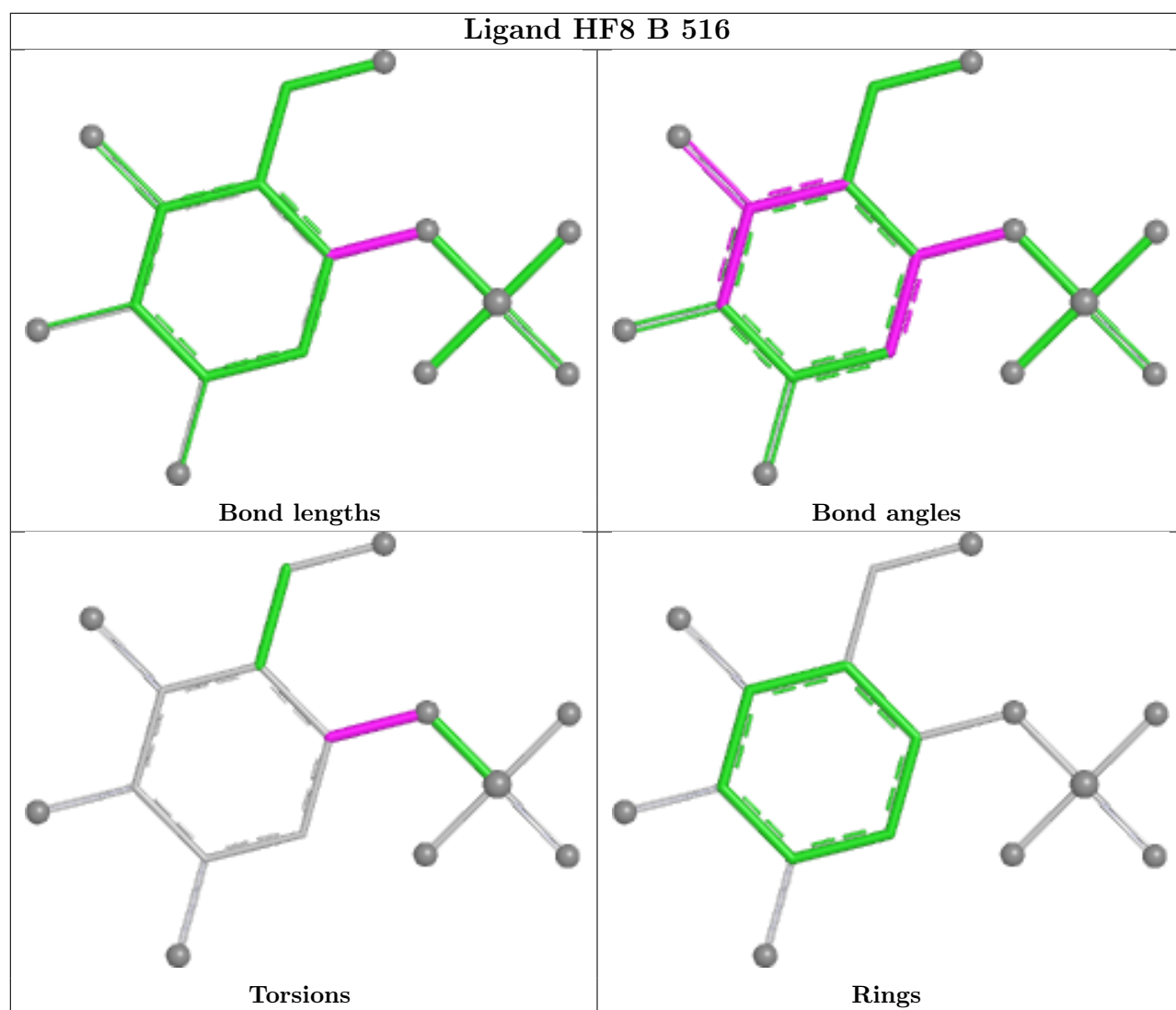
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	510	PEG	1	0
7	B	513	SO4	1	0
6	A	512	ACT	1	0
7	A	514	SO4	1	0
5	A	509	PEG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand HF8 A 517





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	390/398 (97%)	-0.11	0 100 100	22, 53, 70, 100	10 (2%)
1	B	392/398 (98%)	0.16	4 (1%) 79 82	42, 59, 86, 116	4 (1%)
All	All	782/796 (98%)	0.02	4 (0%) 87 89	22, 55, 80, 116	14 (1%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	LYS	3.3
1	B	209	TRP	3.1
1	B	421	MET	2.1
1	B	150	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	G	2	14/15	0.43	0.13	130,139,143,155	0
2	NAG	H	2	14/15	0.48	0.12	112,124,137,140	0
2	BMA	H	3	11/12	0.52	0.11	122,136,146,150	0
2	BMA	C	3	11/12	0.54	0.14	94,106,119,128	0
2	BMA	E	3	11/12	0.59	0.10	114,124,137,137	0

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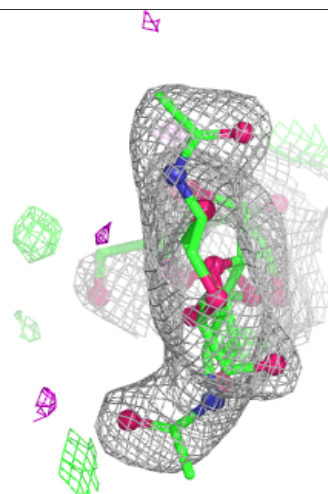
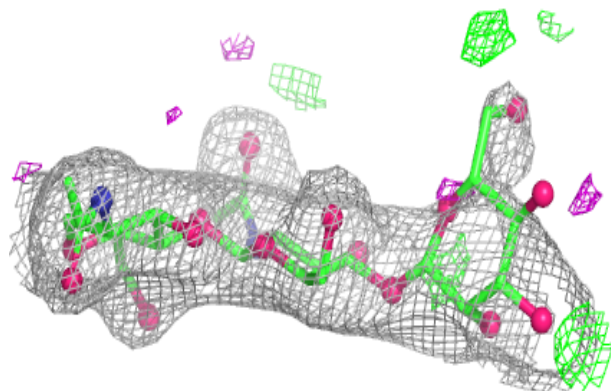
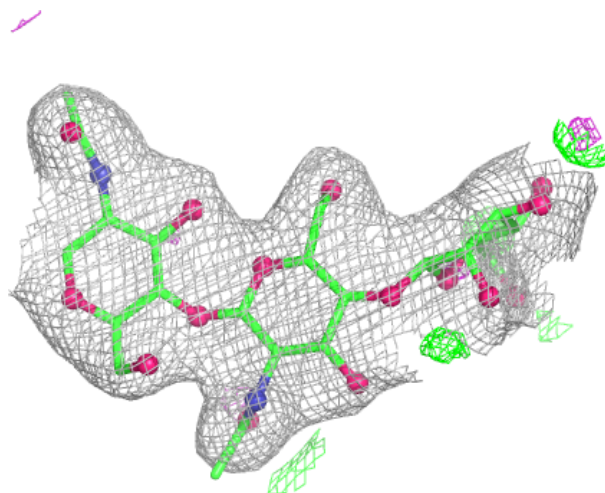
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MAN	F	6	11/12	0.59	0.11	95,111,121,121	0
4	MAN	F	5	11/12	0.65	0.08	125,134,139,150	0
3	NAG	D	2	14/15	0.73	0.11	91,100,106,109	0
2	NAG	E	2	14/15	0.75	0.11	91,104,119,130	0
4	MAN	F	4	11/12	0.82	0.09	82,100,112,117	0
3	NAG	G	1	14/15	0.82	0.10	83,107,117,126	0
4	BMA	F	3	11/12	0.82	0.08	75,95,105,106	0
2	NAG	H	1	14/15	0.84	0.11	78,102,112,120	0
2	NAG	E	1	14/15	0.85	0.10	71,81,87,91	0
4	NAG	F	1	14/15	0.87	0.09	64,74,83,83	0
3	NAG	D	1	14/15	0.89	0.09	72,76,94,96	0
4	NAG	F	2	14/15	0.89	0.08	79,85,89,89	0
2	NAG	C	2	14/15	0.92	0.08	62,79,91,96	0
2	NAG	C	1	14/15	0.96	0.07	57,61,66,68	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

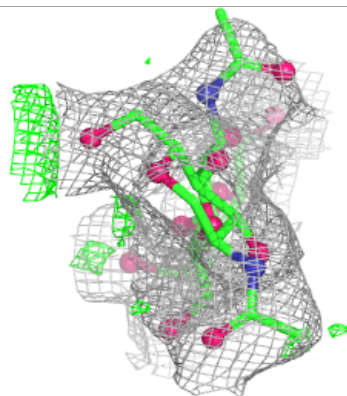
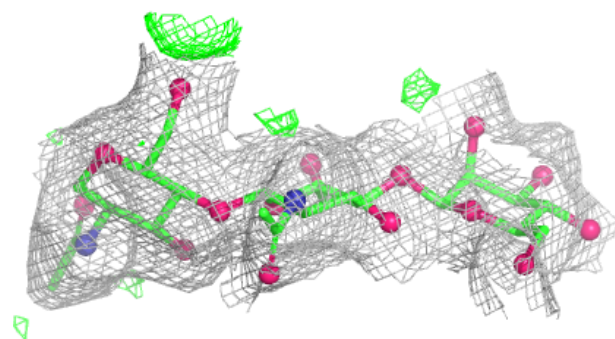
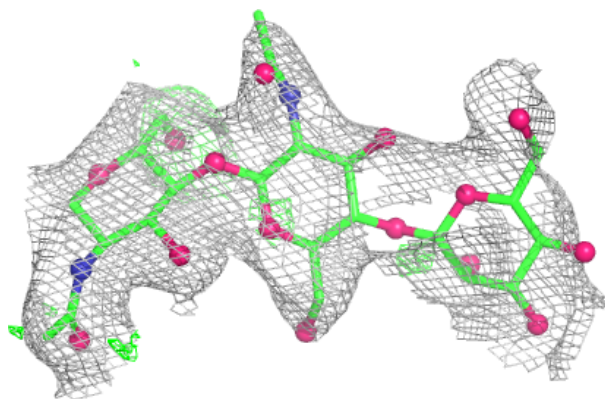
Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



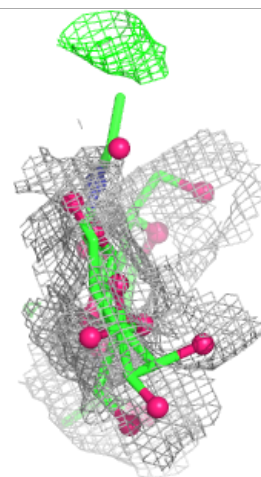
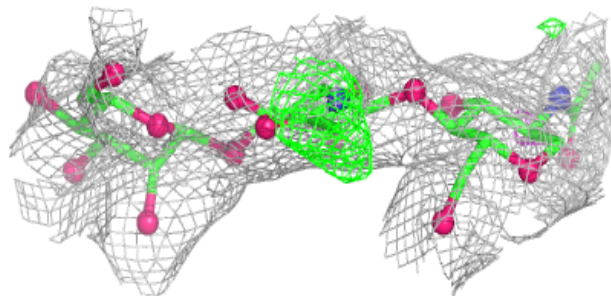
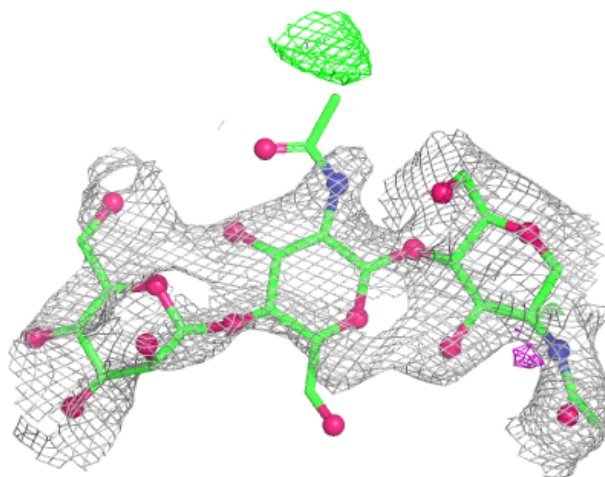
Electron density around Chain E:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



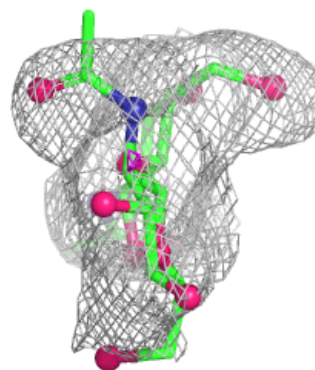
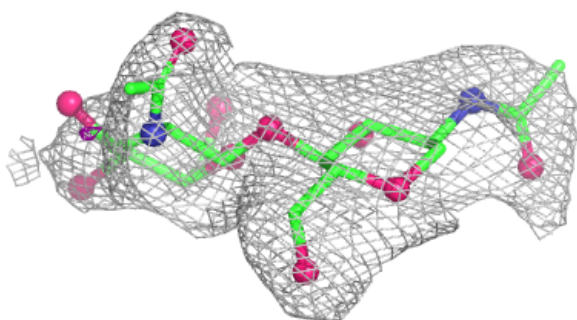
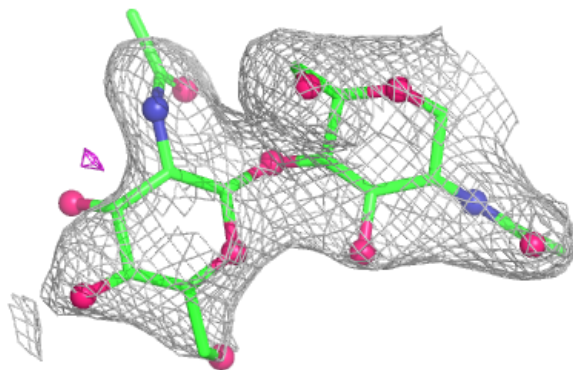
Electron density around Chain H:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



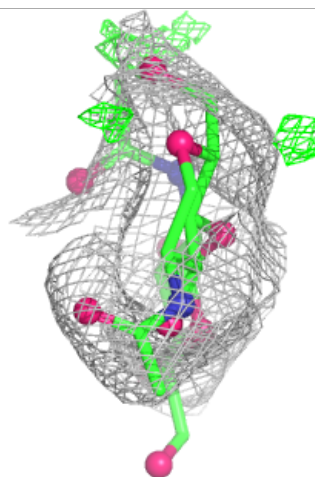
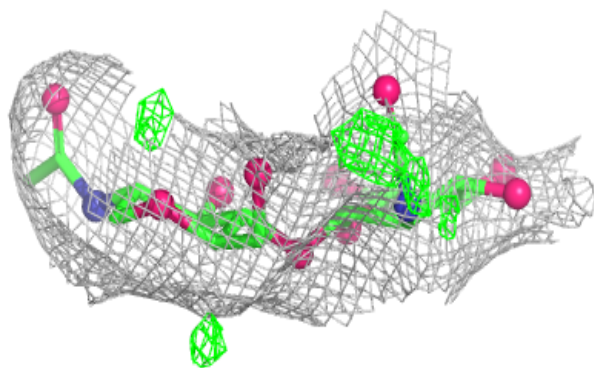
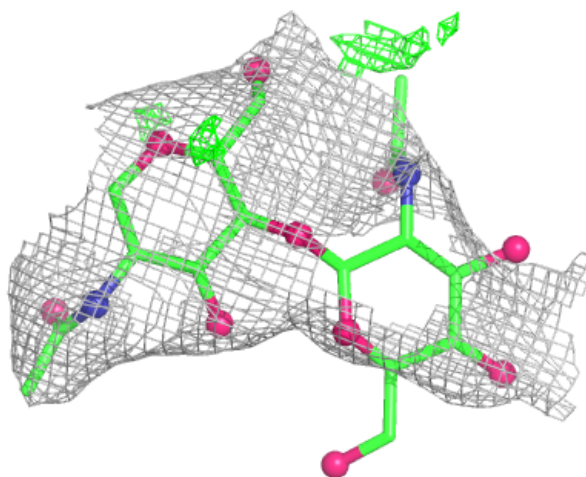
Electron density around Chain D:

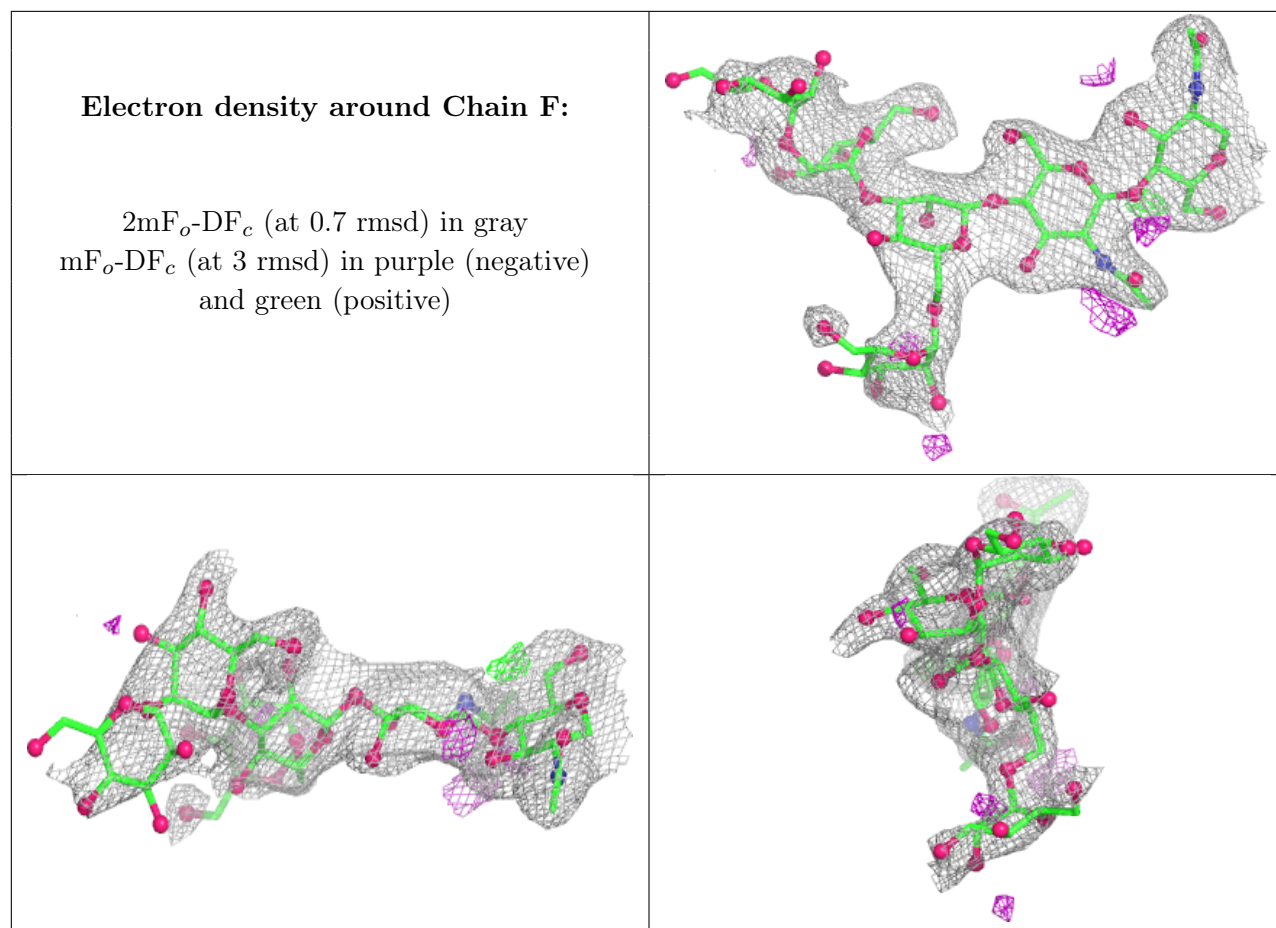
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	EDO	B	518	4/4	0.63	0.15	91,94,95,95	0
5	PEG	A	510	7/7	0.64	0.23	65,87,91,93	0
9	EDO	B	525	4/4	0.73	0.12	85,98,102,106	0
6	ACT	A	511	4/4	0.75	0.13	82,91,92,96	0
6	ACT	A	513	4/4	0.77	0.22	69,78,78,87	0
6	ACT	B	512	4/4	0.78	0.13	77,81,84,86	0
7	SO4	B	515	5/5	0.78	0.07	122,123,129,142	0
7	SO4	A	516	5/5	0.79	0.08	94,102,118,120	0
9	EDO	B	521	4/4	0.80	0.18	90,94,97,104	0
9	EDO	B	520	4/4	0.82	0.14	84,87,89,99	0
9	EDO	A	518	4/4	0.82	0.16	64,67,70,70	0
6	ACT	A	512	4/4	0.82	0.16	57,68,72,76	0

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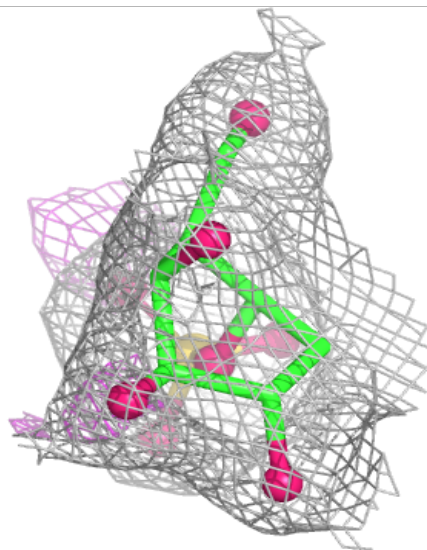
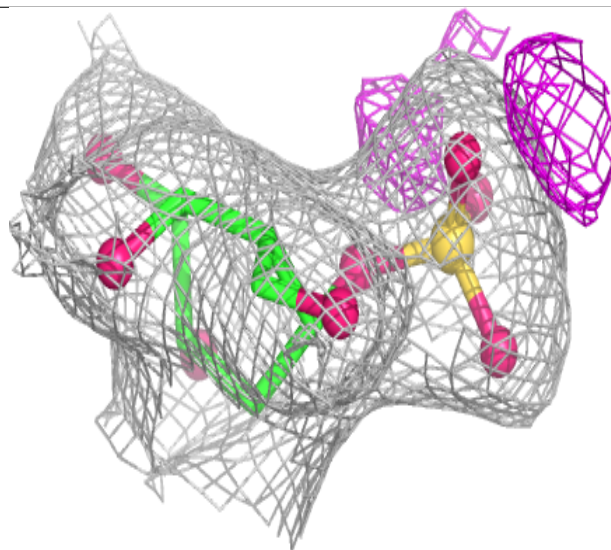
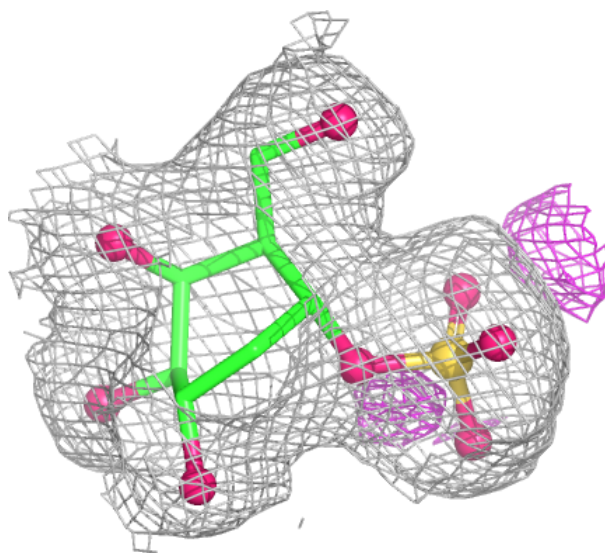
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	EDO	A	526	4/4	0.84	0.19	74,83,84,84	0
9	EDO	B	524	4/4	0.86	0.15	74,75,77,83	0
5	PEG	A	509	7/7	0.87	0.13	63,71,75,86	0
9	EDO	B	523	4/4	0.87	0.15	69,74,75,76	0
9	EDO	A	522	4/4	0.88	0.15	63,75,77,80	0
9	EDO	A	521	4/4	0.88	0.32	43,45,49,53	4
9	EDO	B	517	4/4	0.89	0.13	78,82,83,83	0
7	SO4	A	515	5/5	0.90	0.08	74,78,81,92	0
9	EDO	A	525	4/4	0.90	0.13	80,81,82,87	0
9	EDO	A	524	4/4	0.91	0.10	64,80,81,84	0
9	EDO	A	520	4/4	0.92	0.12	61,62,64,72	0
9	EDO	A	519	4/4	0.92	0.12	56,69,70,73	0
9	EDO	B	522	4/4	0.92	0.09	65,70,72,74	0
7	SO4	B	514	5/5	0.93	0.08	58,59,63,66	5
9	EDO	A	523	4/4	0.94	0.13	74,74,75,81	0
9	EDO	B	519	4/4	0.94	0.11	70,73,73,77	0
8	HF8	A	517	16/17	0.95	0.07	45,53,62,68	0
8	HF8	B	516	16/17	0.95	0.06	48,54,64,74	0
7	SO4	B	513	5/5	0.96	0.05	69,72,79,88	0
7	SO4	A	514	5/5	0.97	0.05	63,74,82,83	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

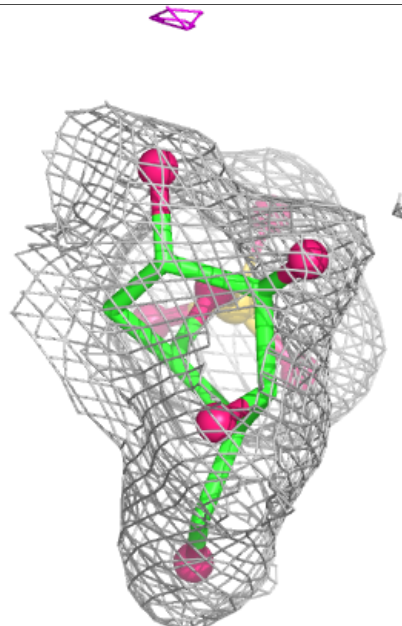
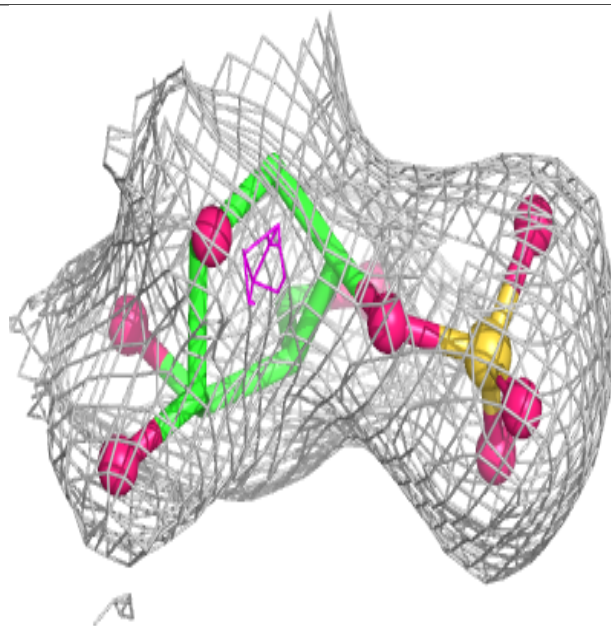
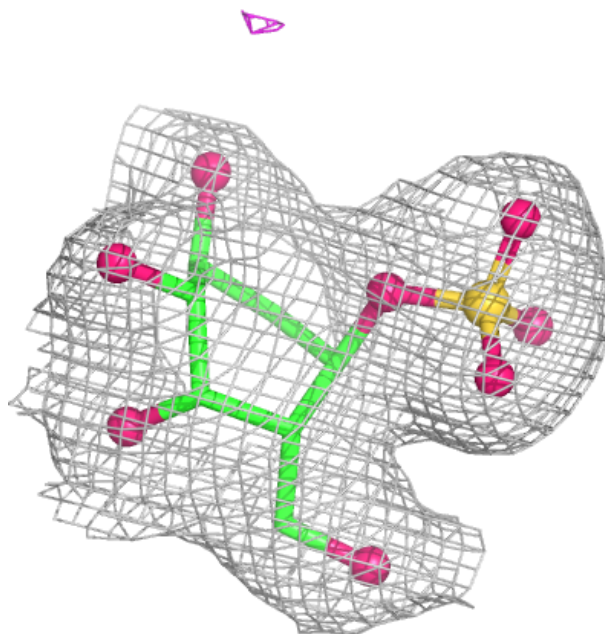
Electron density around HF8 A 517:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HF8 B 516:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.